JAN

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Access DB#

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: My-Chan Train Examiner #: 78933 Date: 3/12/02 Art Unit: 1691 Phone Number 30 5 - 6999 Serial Number: 09/781, 697 Mail Box and Bldg/Room Location: CMI, 8416 Results Format Preferred (circle): PAPER DISK E-MAIL 7612.		
If more than one search is submitted, please prioritize searches in order of need.		
Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.		
Title of Invention: Bioseusor Compositions and Methods of Use		
Title of Invention: Bioseusor Compositions and Methods of Use Inventors (please provide full names): Hagan P. Bayley, Repl Stefan G. Howorka, and Livin Movifean a		
Earliest Priority Filing Date: $2/11/2000$		
For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the		
appropriate serial number.		
Jan, (an you please perform the following searches: 1) Inventors search 2) Search attached claims Jan Delaval Reference Librarian Biotechnology & Chemical Library CM1 1E07-703-308-4498 jan.delaval@uspto.gov		
•	. *	
***********		*********
STAFF USE ONLY	Type of Search	Vendors and cost where applicable STN
Searcher: 4758	NA Sequence (#)	Dialog
Searcher Location:	Structure (#)	Questel/Orbit
Date Searcher Picked Up: 315102	Bibliographic	Dr.Link
Date Completed: 315102	Litigation	Lexis/Nexis
Searcher Prep & Review Time:	Fulltext	Sequence Systems
Clerical Prep Time:	Patent Family	WWW/Internet

PTO-1590 (8-01)

=> fil wpix FILE 'WPIX' ENTERED AT 15:12:17 ON 19 MAR 2002 COPYRIGHT (C) 2002 DERWENT INFORMATION LTD

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
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jan delaval@uspto.gov

FILE LAST UPDATED: 13 MAR 2002 <20020313/UP>
MOST RECENT DERWENT UPDATE 200217 <200217/DW>
DERWENT WORLD PATENTS INDEX SUBSCRIBER FILE, COVERS 1963 TO DATE

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=> d all abeq tech tot

L71 ANSWER 1 OF 6 WPIX COPYRIGHT 2002 DERWENT INFORMATION LTD

AN 2002-026220 [03] WPIX

DNN N2002-020192 DNC C2002-007456

TI Transporting molecule, e.g. pharmaceuticals or glucose, through mammalian barrier membrane e.g. human skin membrane, by ablating membrane with shear device.

DC B07 P34 S05

IN COSTON, A F; KOLLIAS, N; SUN, Y

PA (JOHJ) JOHNSON & JOHNSON CONSUMER CO INC

CYC 93

PI WO 2001083027 A2 20011108 (200203)* EN 59p A61N001-30

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW

W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG UZ VN YU ZA ZW

ADT WO 2001083027 A2 WO 2001-US14054 20010501

PRAI US 2001-845956 20010430; US 2000-200839P 20000501

IC ICM A61N001-30

AB WO 200183027 A UPAB: 20020114

NOVELTY - Transporting a molecule through a mammalian barrier membrane comprises ablating the membrane with a shear device having a sheet containing at least one opening and shear blade. The sheet is contacted with the membrane to force a membrane part through the opening and ablate the membrane part exposed through the opening. A driving force is used to move the molecule through the perforated membrane.

USE - Used for transporting a molecule e.g. pharmaceutical including polysaccharides, peptides, protein, polynucleotides, glucose or a vaccine (e.g., vaccine against Staphylococcus aureus) through mammalian barrier membrane e.g., human skin, buccal, vaginal, or rectal membranes. The molecule can be transported from within the mammal out through the membrane.

ADVANTAGE - The method controls the transportation of molecules across barrier membranes. The **pores** created by the shear perforation method are not transient (e.g., in contrast to electroporation), but permanent as these **pores** will remain open until the new cells are re-grown over the opening. The method eliminates the need for constant monitoring of the state of the transient microscopic **pores** as in electroporation.

Dwg.0/9

FS CPI EPI GMPI

FA AB; DCN

MC CPI: B04-C01; B04-C02; B04-N04; B11-C09

EPI: S05-M

TECH UPTX: 20020114

TECHNOLOGY FOCUS - BIOLOGY - Preferred Device: The device also comprises a sensor, which can be pressure, conductivity, impedance, pH, or temperature sensor. A feedback from the sensor modifies the driving unit. The sensor is an impedance sensor for detecting the impedance of the barrier membrane and relaying it to a microprocessor. The shear device comprises a driving unit to move the blade. The driving unit is powered manually or by an electric motor. The membrane portion is forced into the opening by a pressure force, preferably a mechanical pressure or suction.

The driving force is iontophoresis, electro-osmosis, reverse iontophoresis, electroporation, phonophoresis, pressure gradients, or concentration gradients. The sheet blade moves parallel to the sheer sheet.

L71 ANSWER 2 OF 6 WPIX COPYRIGHT 2002 DERWENT INFORMATION LTD

AN 2001-589719 [66] WPIX

DNN N2001-439283 DNC C2001-174819

TI Modified, covalently-linked, sensing **pore**-subunit **polypeptides** useful for detecting and measuring analytes or physical characteristics within a sample, are capable of assembling into **pore** assemblies.

DC A96 B04 S03

IN BAYLEY, H P; HOWORKA, S G; MOVILEANU, L

PA (TEXA) UNIV TEXAS A & M SYSTEM

CYC 93

PI WO 2001059453 A2 20010816 (200166) * EN 90p G01N033-53

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW

W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG UZ VN YU ZA ZW

AU 2001041474 A 20010820 (200175) G01N033-53

ADT WO 2001059453 A2 WO 2001-US4482 20010212; AU 2001041474 A AU 2001-41474 20010212

FDT AU 2001041474 A Based on WO 200159453

PRAI US 2000-182097P 20000211

IC ICM G01N033-53

AB WO 200159453 A UPAB: 20011113

NOVELTY - A modified pore-subunit polypeptide (I)

comprising a pore-subunit polypeptide covalently

linked to at least a sensing moiety, which assembles into an oligomeric pore assembly in the presence of several pore-subunit polypeptides, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following: (1) an oligomeric **pore** assembly (II) comprising several (I) sufficient to form a **pore**; and (2) a **biosensor** device comprising (II).

USE - The modified pore-subunit polypeptides are capable of assembling into pores or oligomeric pore assemblies which are useful for detecting the presence of an analyte, especially an oligonucleotide in a sample, by contacting the sample with (II) and detecting an electrical current through a first channel, where the modulation in current compared to a current measurement in a control sample lacking the analyte indicates the presence of the analyte in the sample. They are useful for detecting and quantitating the presence of an unknown analyte in a sample, by detecting an electric current through single or at least two channels to determine a sample current signature and comparing the signature to a standard current signature of a known analyte, where the concurrence of the sample and standard current signatures indicates identity of unknown analyte. (II) is also useful for detecting a change in the type or amount of biological or chemical constituent in the sample or physical environment of the sample. The method involves contacting the sample with (II) at a two time points,

determining two sample current signatures by detection of an electrical

current through a first channel in continuous flow mode, comparing the sample current signatures, where a difference between the signatures indicates a change in the type or amount of biological or chemical constituent in the sample or physical environment of the sample (claimed). The biosensor devices are useful for detecting changes in ionic current flow, to detect, quantitate and/or discriminate between components driven through the pore by an applied potential and for detecting any analyte, component or physical parameter that contacts or impacts the measurable channel of the pore assembly. Dwg.0/9 CPI EPI FS AB; DCN FA CPI: A12-V03C2; B04-B01B; B04-B03C; B04-C01; B04-C02; B04-C02X; B04-C03C; B04-E01; B04-G01; B04-L01; B06-F03; B11-C08; B12-K04 EPI: S03-E14H4 TECH UPTX: 20011113 TECHNOLOGY FOCUS - BIOTECHNOLOGY - Preferred Polypeptide: (I) is staphylococcal hemolysin polypeptide, porin, complement pore polypeptide, hemolysin C polypeptide or streptolysin O polypeptide, preferably a mutant staphylococcal alpha-hemolysin polypeptide comprising a first heterologous amino acid. The mutant polypeptide comprises a cysteine residue in place of serine at position 106 or lysine at position 8 of the wild-type staphylococcal alpha-hemolysin polypeptide. The sensing moiety is a functional group, such as a synthetic molecule, e.g. calixarene or crown ether, a naturally occurring molecule e.g. enzyme inhibitor, hapten, nucleotide, amino acid, lipid, toxin, saccharide, chelator or cyclodextrin or is a polymer e.g. polyethylene glycol (PEG)-biotin, analyte-binding polymer, oligonucleotide, oligosaccharide or peptide. The sensing moiety binds to a metal, metal ion, toxin, enzyme, nucleotide, oligonucleotide, amino acid, peptide, saccharide, hapten, lipid or antibody or its antigen-binding fragment and responds to a change in the type or amount of a biological or chemical constituent in the environment or physical environment of (II), such as pH, voltage, light or temperature. (I) is covalently linked to same or different sensing moieties. (II) comprises several modified pore -subunit polypeptides, preferably 7 pore-subunit polypeptides. L71 ANSWER 3 OF 6 WPIX COPYRIGHT 2002 DERWENT INFORMATION LTD AN 2000-387818 [33] WPIX DNC C2000-117822 Analytical system for rapid detection and identification of analytes based upon spore germination, comprises using a reaction mixture containing microbial spore which can sense analyte specific signals. DC B04 D16 IN ROTMAN, M B PA (ROTM-I) ROTMAN M B CYC 23 WO 2000029610 A1 20000525 (200033)* EN 37p PΤ C120001-02 RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE W: AU CA JP AU 2000016273 A 20000605 (200042) C12Q001-02 B1 20010508 (200128) C12Q001-00 US 6228574 EP 1131462 A1 20010912 (200155) EN C12Q001-02 R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE ADT WO 2000029610 A1 WO 1999-US27214 19991116; AU 2000016273 A AU 2000-16273 19991116; US 6228574 B1 US 1998-193385 19981117; EP 1131462 A1 EP 1999-959015 19991116, WO 1999-US27214 19991116 FDT AU 2000016273 A Based on WO 200029610; EP 1131462 A1 Based on WO 200029610 PRAI US 1999-134781P 19990519; US 1998-193385 ICM C12Q001-00; C12Q001-02 ICS C12Q001-68; C12Q001-70 AB WO 200029610 A UPAB: 20000712

NOVELTY - A method for detecting the presence of a suspected analyte in a test sample, comprising combining a test sample containing the suspected analyte, with a reaction mixture comprising microbial spores that can sense an analyte-specific signal and respond to it by establishing an analyte-independent signal amplification system, and a germinogenic source, is new.

DETAILED DESCRIPTION - The mixture is incubated to allow enzymatic conversion of the germinogenic source to a germinant, and for spore germination. Spore germination is detected by a measurable parameter, where the suspected analyte is capable of generating a germinant by enzymatic action on the germinogenic source.

USE - The method is used to detect the presence and quantity of specific target analytes, (claimed) e.g. microbes such as bacteria (e.g. Enterobacter aerogenes, Escherichia coli, Chlamydia trachomatis, Clostridium, Haemophilus influenza, Klebsiella pneumoniae, Neisseria gonorrhoeae, Salmonella, and Staphylococcus), fungi (e.g. Aspergillus fumigatus, Blastomyces dermatitidis, Candida albicans, and Trichomonas vaginalis) and protozoa, viruses (e.g. cytomegalovirus, hepatitis virus, herpes virus, and human immunodeficiency virus), nucleic acid macromolecules (e.g. DNA or RNA), proteins, and naturally soluble macromolecules (e.g. chemokines, cytokines, growth factors, hormones). The analyte must be capable of generating a germinant by enzymatic action on a germinogenic source.

ADVANTAGE - The present invention reduces the time and cost of prior art analytical tools, resulting in faster diagnosis. The invention does not require growth of vegetative bacterial cells since it depends exclusively on spore germination, and does not require enzyme-labeled probes.

DESCRIPTION OF DRAWING(S) - The figure is a diagrammatical view of a **biosensor** used in the invention. The figure includes a top view and two cross-sectional views of portions of the **biosensor**.

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Biosensor 10
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Mesh 12

Membrane filter 14

0.2 mu m pores 15

Microwells 16

Suspension 18.

Dwg.1/1

FS CPI

FA AB; GI; DCN

4C CPI: B04-E02; B04-F06; B04-F09A; B04-F10; B04-F10A3; B04-F10A5; B04-F10A8; B04-F10B3; B04-F11; B04-H01; B04-H06; B04-L01; B11-C08E1; D05-A02; D05-H04; D05-H05; D05-H06; D05-H09

TECH UPTX: 20000712

TECHNOLOGY FOCUS - BIOTECHNOLOGY - Preferred Method: The microbial spores can be natural, or genetically modified to a carry a chromosomal gene selected from a lux bioluminescence gene which only becomes bioluminescent upon germination, a lac gene which only produces a reporter enzyme upon germination, and a fluorescent protein coding gene which only produces the fluorescent protein upon germination. The spores are produced by bacteria or fungi. The germinant source is converted to the germinant by contact with at least one enzyme. Alternatively, a complex germinogenic source is used where an enzyme generates a reaction product which is converted into a germinant in the presence of one or more addition molecules. The suspected analyte is initially incapable of generating a germinant by enzymatic reaction on a germinogenic source, and becomes capable during the method, or by means of a germinogenic enzyme attached to the analyte. The analyte naturally produces an enzyme which results in the enzymatic conversion of the germinogenic source to germinant. Prior to combining, the spores are processed to be devoid of active germinant. Detection is by loss of spore biofringence, or by the appearance of enzymatic activity due to an enzyme which is synthesized de novo or activated in the germinating spores.

TECHNOLOGY FOCUS - BIOLOGY - Preferred Analyte: The suspected analyte is a microbe, virus, an insoluble nucleic acid macromolecule, or naturally

soluble macromolecule which has been immobilized in or on discrete particles. The analyte us DNA specifically labeled using complementary oligonucleotides linked to a germinogenic enzyme by biotin-avidin bonds.

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L71 ANSWER 4 OF 6 WPIX
                          COPYRIGHT 2002
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AN
     1999-153311 [13]
                        WPIX
DNN N1999-110551
                        DNC C1999-045198
ΤI
     New mutant staphylococcal alpha-haemolysin - comprises
     a heterologous amino acid that binds to analyte, particularly metal ions.
DC
     B04 D15 D16 E19 E37 J04 K04 S03
TN
    BAYLEY, H; BRAHA, O; GOUAUX, E; KASIANOWICZ, J
     (UYMA-N) UNIV MASSACHUSETTS
PA
CYC 22
                   A1 19990204 (199913) * EN
                                              50p
PΤ
    WO 9905167
                                                     C07K014-195
        RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE
        W: AU CA JP KR
     AU 9885862
                   A 19990216 (199926)
                                                     C07K014-195
ADT
    WO 9905167 A1 WO 1998-US15354 19980724; AU 9885862 A AU 1998-85862
     19980724
FDT AU 9885862 A Based on WO 9905167
PRAI US 1997-53737P
                    19970725
TC
     ICM C07K014-195
     ICS C07K014-305; C07K014-31; G01N033-20; G01N033-48
AB
          9905167 A UPAB: 19990331
     New mutant staphylococcal alpha -haemolysin (aHL)
     polypeptide (I): (i) includes a heterologous amino acid (HAA) that
     binds an analyte, and (ii) assembles into a heteroheptameric pore
     assembly in presence of many wild-type aHL polypeptides. Also
     new are: (1) aHL polypeptide (Ia) with at least two
     non-consecutive HAA in its stem domain, each of which binds: (i) a metal,
     or (ii) an organic compound; (2) heptameric pore assemblies
     (HPA) containing (I), and (3) digital biosensors comprising HPA.
          USE - The biosensors are particularly used to detect and
     quantify metal ions (specifically zinc, cobalt, nickel and cadmium), e.g.
     in water (for micronutrient analysis), sediment, air, industrial effluent.
     Organic compounds that can be detected are specifically explosives, but
     may also be macromolecules or entire bacteria or viruses.
          ADVANTAGE - Pore-forming bacterial proteins such
     as aHL are robust and provide an information-rich signal by single-channel
     recording. The binding site in (I) need not be strictly specific, since
     the kinetics, extent and voltage-dependence of the channel blockade
     provides a differential analysis, allowing several measurements to be made
     simultaneously. Compared with conventional analogue/steady state
    biosensors, the new devices have a much wider dynamic range (over
     10000-fold, compared with about 20-fold, since the quality of the signal
     is independent of site occupancy and simultaneous occupation with
     different analytes can not occur). The digital mode allows operation in
     real chemical time and the biosensors are sensitive (in the
     nanomolar range), rapid, reversible and selective.
     Dwg.0/8
FS
    CPI EPI
FA
    AB; DCN
MC.
    CPI: B04-C01; B04-F10; B04-F11; B04-N02; B05-A03A; B12-K04;
          D05-H04; D05-H06; E10-B02D; E35-C; J04-C04; K04-F
     EPI: S03-E14C; S03-E14H
L71 ANSWER 5 OF 6 WPIX
                           COPYRIGHT 2002
                                            DERWENT INFORMATION LTD
AN
                        WPIX
    1996-251085 [25]
     1995-014066 [02]
CR
DNC
    C1996-079455
     Prepn. of synthetic ion channels - by coupling active ion channel peptide
     sub units to a polypeptide backbone.
DC
     B04 J04
    MONTAL, M; TOMICH, J
IN
```

(SYNP-N) SYNPORIN TECHNOLOGIES INC

PA (: CYC 1

```
A 19960514 (199625)*
                                              31p
                                                    A61K038-04
    US 5516890
PΙ
ADT US 5516890 A CIP of US 1989-430814 19891102, Div ex US 1990-576222
     19900831, US 1994-312821 19940927
FDT US 5516890 A Div ex US 5368712
PRAI US 1990-576222 19900831; US 1989-430814 19891102; US 1994-312821
     19940927
     ICM A61K038-04
IC
     ICS C07K005-00; C07K007-00
          5516890 A UPAB: 19960625
AR
     (A) A sequential method for prepg. a polypeptide backbone and
     active ion channel subunits comprises (a) prepg. a polypeptide
     backbone portion having 1-10 amino acids, (b) reacting a terminal NH2 gp.
     of the backbone portion with a first t-Boc and Fmoc substd. amino acid,
     (c) deprotecting the t-Boc NH2 residue, (d) introducing an active
     peptide subunit onto the t-Boc deprotected NH2 residue, (e)
     deprotecting the Fmoc NH2 residue, (f) introducing a backbone
     protein sequence onto the deprotected Fmoc NH2 residue, (g)
     reacting a second t-Boc and Fmoc substd. amino acid and backbone terminal
     NH2 residue, (h) deprotecting the t-Boc NH2 residue of the second Fmoc and
     t-Boc substd. amino acid, and (i) introducing an active peptide
     subunit onto the deprotected t-Boc NH2 residue. Also claimed are (B) a
     peptide comprising D-P-W-N-V-F-D-F-L-I-V-I-S-S-I-I-D-V-I-L-S-G (I)
     or A-R-T-V-F-G-V-T-T-V-L-T-M-T-T-L-S-T-S-A-R (II); and (C) a
     peptide template comprising B'[(X)nB']m (III) or (X)n[B'(X)n]m
     (IV), in which B' = a basic amino acid having a terminal amino gp. which
     is bound to a protective gp., X = any arbitrary amino acid, and m and n =
          USE - The synthetic channel ion proteins can be used for
     testing properties of pharmacological cpds. or for the presence of
     particular cpds. or characteristics. They are used partic. for the prodn.
     of biosensors.
          ADVANTAGE - The synthetic polypeptides have a sequence
     ordered to form an active interior pore surface with surrounding
     molecular structures such that they have response characteristics mimetic
     to a chosen native channel even though the synthetic channel does not
     comprise the whole native channel but uses only selected subunits.
     Dwg.0/15
     CPT
FS
     AB; DCN
FΑ
     CPI: B04-C01; B04-N04A; B11-C08; B12-K04; J04-B01B; J04-C04
                                            DERWENT INFORMATION LTD
L71 ANSWER 6 OF 6 WPIX COPYRIGHT 2002
                        WPIX
ΑN
     1995-014066 [02]
     1996-251085 [25]
CR
                        DNC C1995-006313
DNN N1995-010995
     Synthetic ion channel assembly contg. synthetic protein - comprising
ΤI
     template and tethered peptide chains incorporated into lipid bi layer,
     accurately mimicking native channels, and bio sensor
      (s) based on it.
     B04 J04 S03
DC
     MONTAL, M; TOMICH, J
 IN
     (SYNP-N) SYNPORIN TECHNOLOGIES INC
 PA
CYC 1
                                                      G01N027-327
                   A 19941129 (199502)*
PΙ
     US 5368712
ADT US 5368712 A CIP of US 1989-430814 19891102, US 1990-576222 19900831
PRAI US 1990-576222 19900831; US 1989-430814
                                                 19891102
     ICM G01N027-327
 IC
          5368712 A UPAB: 19960705
 AB
     US
      A novel synthetic assembly for in vitro active ion transport, mimicking a
      native ion channel, comprises: (1) electrically insulating membrane; and
      (2) many synthetic protein units (I), transmembranely dispersed
      in the membrane, each (I) contg. a template peptide (TP) and
      4-10 polypeptide subunits (Ia) tethered to it, mimicking an
      active part of a native ion channel protein and positioned to
      extend from TP through the membrane. These structures define (a) a gated
```

ion channel pore and (b) a detector region associated with the

pore.

USE - The **biosensors** are used for in vitro detection, and determn., of physiologically active substances such as antiseptics, antibiotics and neurotransmitters, also toxins, insecticides, food additives, etc..

ADVANTAGE - These synthetic channels are less expensive than native structures but still provide a response that accurately represents physiological response. (I) are self-assembling, stable and robust, and can be prepd. in any desired quantity.

Dwg.7/15

FS CPI EPI

FA AB; DCN

MC CPI: B04-C01; B04-N02; B05-A01A; B05-A01B; B10-B02; B11-C08B;

B11-C08E; B12-K04A; J04-C04

EPI: S03-E03C; S03-E14H

=> fil hcaplus

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FILE COVERS 1907 - 19 Mar 2002 VOL 136 ISS 12 FILE LAST UPDATED: 18 Mar 2002 (20020318/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

CAS roles have been modified effective December 16, 2001. Please check your SDI profiles to see if they need to be revised. For information on CAS roles, enter HELP ROLES at an arrow prompt or use the CAS Roles thesaurus (/RL field) in this file.

The P indicator for Preparations was not generated for all of the CAS Registry Numbers that were added to the CAS files between 12/27/01 and 1/23/02. As of 1/23/02, the situation has been resolved. Searches and/or SDIs in the H/Z/CA/CAplus files incorporating CAS Registry Numbers with the P indicator executed between 12/27/01 and 1/23/02 may be incomplete. See the NEWS message on this topic for more information.

=> d all tot

L82 ANSWER 1 OF 24 HCAPLUS COPYRIGHT 2002 ACS

AN 2001:871429 HCAPLUS

TI Prolonged residence time of a noncovalent molecular adapter, .beta.-cyclodextrin, within the lumen of mutant .alpha.-hemolysin pores

AU Gu, Li-Qun; Cheley, Stephen; Bayley, Hagan

- CS Department of Medical Biochemistry and Genetics, The Texas A and M University System Health Science Center, College Station, TX, 77843, USA
- SO J. Gen. Physiol. (2001), 118(5), 481-493 CODEN: JGPLAD; ISSN: 0022-1295
- PB Rockefeller University Press

DT Journal

```
LA
     English
CC
     7 (Enzymes)
     Noncovalent mol. adapters, such as cyclodextrins, act as binding sites for
AB
     channel blockers when lodged in the lumen of the .alpha.-
     hemolysin (.alpha.HL) pore, thereby offering a
     basis for the detection of a variety of org. mols. with .alpha
     .HL as a sensor element. .beta.-Cyclodextrin (.beta.CD) resides
     in the wild-type .alpha.HL pore for several hundred
     microseconds. The residence time can be extended to several milliseconds
     by the manipulation of pH and transmembrane potential. Here, we describe
     mutant homoheptameric .alpha.HL pores that are capable
     of accommodating .beta.CD for tens of seconds. The mutants were obtained
     by site-directed mutagenesis at position 113, which is a residue that lies
     near a constriction in the lumen of the transmembrane .beta. barrel, and
     fall into two classes. Members of the tight-binding class, M113D, M113N,
     M113V, M113H, M113F and M113Y, bind .beta.CD .apprx.104-fold more avidly
     than the remaining .alpha.HL pores, including \overline{\text{WT-}}.
     alpha. HL. The lower Kd values of these mutants are dominated by
     reduced values of koff. The major effect of the mutations is most likely
     a remodeling of the binding site for .beta.CD in the vicinity of position
     113. In addn., there is a smaller voltage-sensitive component of the
     binding, which is also affected by the residue at 113 and may result from
     transport of the neutral .beta.CD mol. by electroosmotic flow. The mutant
     pores for which the dwell time of .beta.CD is prolonged can serve
     as improved components for stochastic sensors.
               THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD
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AN 2001:858309 HCAPLUS

DN 136:130977

- Kinetics of duplex formation for individual DNA strands within a single protein nanopore Howorka, Stefan; Movileanu, Liviu; Braha, Orit; ΑU Bayley, Hagan Department of Medical Biochemistry and Genetics, The Texas A and M CS University System Health Science Center, College Station, TX, 77843-1114, Proceedings of the National Academy of Sciences of the United States of SO America (2001), 98(23), 12996-13001 CODEN: PNASA6; ISSN: 0027-8424 National Academy of Sciences PΒ DT Journal English LΑ CC 9-2 (Biochemical Methods) A single oligonucleotide was covalently attached to a genetically engineered subunit of the heptameric protein pore, .alpha.-hemolysin, to allow DNA duplex formation inside the pore lumen. Single-channel current recording was used to study the properties of the modified pore. On addn. of an oligonucleotide 8 bases in length and with a sequence complementary to the tethered DNA strand, current blockades with durations of hundreds of milliseconds occurred, representing hybridization events of individual oligonucleotides to the tethered DNA strand. Kinetic consts. for DNA duplex formation at the single mol. level were derived and found to be consistent with established literature values for macroscopic duplex formation. The resultant equil. const. for duplex formation in the nanopore was found to be close to the exptl. derived const. for duplex formation in soln. A good agreement between the equil. consts. for duplex formation in the nanopore and in soln. was also found for two other oligonucleotide pairs. In addn., the nanopore recordings revealed details of the kinetics difficult to obtain by conventional methods, like surface plasmon resonance, which measure ensemble properties. By investigating the temp. dependence of DNA duplex formation at the single mol. level, the std. enthalpy and entropy of the interaction could be obtained. DNA duplex formation kinetics hemolysin alpha nanopore ST TΤ DNA RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study) (double-stranded; kinetics of duplex formation for individual DNA strands within a single **protein** nanopore) IT Free energy Molecular association (kinetics of duplex formation for individual DNA strands within a single protein nanopore) ΙT (surface plasmon-based; kinetics of duplex formation for individual DNA strands within a single protein nanopore) TΨ Hemolysins RL: BSU (Biological study, unclassified); BIOL (Biological study) (.alpha.-; kinetics of duplex formation for individual DNA strands within a single protein nanopore) 392247-81-3 392247-83-5 392247-84-6 354584-63-7 ΙT 354584-62-6 392247-85-7 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study) (kinetics of duplex formation for individual DNA strands within a single **protein** nanopore)
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- AN 2001:708018 HCAPLUS
- DN 135:238715
- TI Stochastic sensors inspired by biology
- AU Bayley, Hagan; Cremer, Paul S.
- CS Department of Medical Biochemistry and Genetcs, The Texas A and M University System Health Science Center, College Station, TX, 72843-1114, USA
- SO Nature (London, United Kingdom) (2001), 413(6852), 226-230 CODEN: NATUAS; ISSN: 0028-0836
- PB Nature Publishing Group
- DT Journal; General Review
- LA English
- CC 9-0 (Biochemical Methods)
 - Section cross-reference(s): 1, 4
 A review with apprx.54 refs. S
- AB A review with .apprx.54 refs. Sensory systems use a variety of membrane-bound receptors, including responsive ion channels, to discriminate between a multitude of stimuli. Here we describe how engineered membrane pores can be used to make rapid and sensitive biosensors with potential applications that range from the detection of biol. warfare agents to pharmaceutical screening.

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Notably, use of the engineered pores in stochastic sensing, a
     single-mol. detection technol., reveals the identity of an analyte as well
     as its concn.
     stochastic sensor review
ST
TT
     Biosensors
        (stochastic sensors inspired by biol.)
     Ion channel
TT
     Sensory receptors
     RL: ARU (Analytical role, unclassified); ANST (Analytical study)
        (stochastic sensors inspired by biol.)
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AN
DN
     135:177670
     Biosensors with pore peptide compositions
ΤI
     and methods of use
     Bayley, Hagan P.; Howorka, Stefan G.; Movileanu,
ΙN
     Liviu
     The Texas A + M University System, USA
PΑ
     PCT Int. Appl., 90 pp.
SO
     CODEN: PIXXD2
DΤ
     Patent
     English
LA
     ICM G01N033-53
IC
     9-1 (Biochemical Methods)
FAN.CNT 1
                                            APPLICATION NO. DATE
     PATENT NO.
                      KIND DATE
                                            _____
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                                            WO 2001-US4482
                                                              20010212
                       A2
                            20010816
     WO 2001059453
PΙ
         W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,
             HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT,
             LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU,
             SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU,
             ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
         RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
             DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
             BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
                             20000211
PRAI US 2000-182097P
                       Ρ
     The present invention relates generally to detection of one or more
     analytes in a sample and/or the magnitude of or changes in phys.
     properties of a sample. More particularly, it concerns pore
     -subunit polypeptides covalently linked to one or more sensing
     moieties, and the use of these modified polypeptides to detect
     and/or measure analytes or certain phys. characteristics within a given
     sample. Provided are pore-subunit polypeptides
     covalently linked to one or more sensing moieties, and uses of these
     modified polypeptides as described.
     biosensor pore modified polypeptide
ST
      staphylococcal hemolysin polymer
     Biosensors
ΙT
      Chelating agents
      Functional groups
      Ions
      Light
      Molecular association
      Molecular recognition
      Temperature
      рН
         (Biosensors with pore peptide compns. and
         methods of use)
 IT
      DNA
      RL: ANT (Analyte); ANST (Analytical study)
         (Biosensors with pore peptide compns. and
         methods of use)
      Amino acids, analysis
 IT
      Haptens
      Lipids, analysis
      Nucleotides, analysis
        Oligonucleotides
        Oligosaccharides, analysis
        Peptides, analysis
      Toxins
      RL: ANT (Analyte); ARG (Analytical reagent use); DEV (Device component
      use); ANST (Analytical study); USES (Uses)
         (Biosensors with pore peptide compns. and
```

```
methods of use)
IT
    Antibodies
    Crown ethers
    Enzymes, uses
      Hemolysins O
    Metals, uses
     Polymers, uses
     Polyoxyalkylenes, uses
     Polysaccharides, uses
     Porins
     RL: ARG (Analytical reagent use); DEV (Device component use); ANST
     (Analytical study); USES (Uses)
        (Biosensors with pore peptide compns. and
        methods of use)
ΙT
     Hemolysins
     RL: ARG (Analytical reagent use); DEV (Device component use); ANST
     (Analytical study); USES (Uses)
        (C; Biosensors with pore peptide compns.
        and methods of use)
ΙT
     Metacyclophanes
     RL: ARG (Analytical reagent use); DEV (Device component use); ANST
     (Analytical study); USES (Uses)
        (calixarenes; Biosensors with pore peptide
        compns. and methods of use)
TΤ
     Enzymes, uses
     RL: ARG (Analytical reagent use); DEV (Device component use); ANST
     (Analytical study); USES (Uses)
        (inhibitors; Biosensors with pore peptide
        compns. and methods of use)
     Proteins, general, uses
IT
     RL: ARG (Analytical reagent use); DEV (Device component use); ANST
     (Analytical study); USES (Uses)
        (polypeptide; Biosensors with pore
        peptide compns. and methods of use)
ΙT
     Complement
     RL: ARG (Analytical reagent use); DEV (Device component use); ANST
     (Analytical study); USES (Uses)
        (pore; Biosensors with pore
        peptide compns. and methods of use)
IT
     Hemolysins
     RL: ARG (Analytical reagent use); DEV (Device component use); ANST
     (Analytical study); USES (Uses)
        (staphylococcal; Biosensors with pore
        peptide compns. and methods of use)
     Proteins, specific or class
     RL: ARG (Analytical reagent use); DEV (Device component use); ANST
     (Analytical study); USES (Uses)
        (transmembrane, pore; Biosensors with pore
        peptide compns. and methods of use)
IT
     Hemolysins
     RL: ARG (Analytical reagent use); DEV (Device component use); ANST
      (Analytical study); USES (Uses)
        (.alpha.-, staphylococcal, mutant, with cysteine at
        position 106; Biosensors with pore peptide
        compns. and methods of use)
ΙT
     Hemolysins
     RL: ARG (Analytical reagent use); DEV (Device component use); ANST
      (Analytical study); USES (Uses)
         (.alpha.-, staphylococcal, mutant, with cysteine at
        position 8; Biosensors with pore peptide
        compns. and methods of use)
     Hemolysins
     RL: ARG (Analytical reagent use); DEV (Device component use); ANST
      (Analytical study); USES (Uses)
         (.alpha.-, staphylococcal; Biosensors
        with pore peptide compns. and methods of use)
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12619-70-4, cyclodextrin 25322-68-3, Polyethylene glycol
TΤ
    RL: ARG (Analytical reagent use); DEV (Device component use); ANST
     (Analytical study); USES (Uses)
        (Biosensors with pore peptide compns. and
        methods of use)
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    354648-02-5
                   354648-03-6 354648-04-7
    SEOID: 7 unclaimed DNA 354807-78-6, 3: PN: W00159453 SEQID: 8 unclaimed
         354807-80-0, 4: PN: WO0159453 SEQID: 9 unclaimed DNA 354807-82-2,
    6: PN: WOO159453 SEQID: 11 unclaimed DNA
                                               354807-83-3, 7: PN: WO0159453
    SEQID: 12 unclaimed DNA 354807-84-4, 8: PN: WO0159453 SEQID: 13
                    354807-87-7, 9: PN: WO0159453 SEQID: 14 unclaimed DNA
    unclaimed DNA
    RL: PRP (Properties)
        (unclaimed nucleotide sequence; biosensors with pore
       peptide compns. and methods of use)
                                 354584-63-7
                                               354584-64-8
                  354584-62-6
TΤ
    354584-61-5
    RL: PRP (Properties)
        (unclaimed sequence; biosensors with pore
        peptide compns. and methods of use)
L82 ANSWER 5 OF 24 HCAPLUS COPYRIGHT 2002 ACS
    2001:495050 HCAPLUS
ΑN
DN
    136:145702
     Sequence-specific detection of individual DNA strands using engineered
TΙ
    Howorka, Stefan; Cheley, Stephen; Bayley, Hagan
AU
    Department of Medical Biochemistry and Genetics, The Texas Ae&M University
CS
     System Health Science Center, College Station, TX, 77843-1114, USA
    Nature Biotechnology (2001), 19(7), 636-639 CODEN: NABIF9; ISSN: 1087-0156
SO
PB
    Nature America Inc.
DΤ
    Journal
LA
    English
CC
    3-1 (Biochemical Genetics)
    We describe biosensor elements that are capable of identifying
     individual DNA strands with single-base resoln. Each biosensor
     element consists of an individual DNA oligonucleotide covalently
     attached within the lumen of the c-hemolysin (acHL) pore
     to form a "DNA-nanopore". The binding of single-stranded DNA (ssDNA)
    mols. to the tethered DNA strand causes changes in the ionic current
     flowing through a nanopore. On the basis of DNA duplex lifetimes, the
     DNA-nanopores are able to discriminate between individual DNA strands up
     to 30 nucleotides in length differing by a single base substitution. This
    was exemplified by the detection of a drug resistance-conferring mutation
     in the reverse transcriptase gene of HIV. In addn., the approach was used
     to sequence a complete codon in an individual DNA strand tethered to a
ST
    biosensor alpha hemolysin nanopore
     oligonucleotide conjugate sequencing mutation detection
ΙT
     DNA sequence analysis
     Nucleic acid hybridization
        (sequence-specific detection of individual DNA strands using engineered
TΨ
     DNA
     RL: ANT (Analyte); ANST (Analytical study)
        (sequence-specific detection of individual DNA strands using engineered
        nanopores)
ΙT
     Hemolysins
     RL: ARG (Analytical reagent use); DEV (Device component use); ANST
     (Analytical study); USES (Uses)
        (.alpha.-, nanopores, oligonucleotide conjugates;
        sequence-specific detection of individual DNA strands using engineered
        nanopores)
IT
     Biosensors
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(.alpha.-hemolysin nanopore-oligonucleotide

using engineered nanopores)

conjugate-contg.; sequence-specific detection of individual DNA strands

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9068-38-6, Reverse transcriptase
     RL: BSU (Biological study, unclassified); BIOL (Biological study)
        (HIV, drug resistance-conferring mutation in gene for;
        sequence-specific detection of individual DNA strands using engineered
        nanopores)
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     2001:209001 HCAPLUS
AN
DN
     135:368679
ΤI
    Microfinishing of channel pore and real time sensing
AΠ
     Futaki, Shiro
CS
     Institute for Chemical Research, Kyoto University, Japan
     Kagaku (Kyoto, Japan) (2001), 56(3), 58-59
SO
     CODEN: KAKYAU; ISSN: 0451-1964
PB
     Kagaku Dojin
     Journal; General Review
DΤ
T.A
     Japanese
CC
     9-0 (Biochemical Methods)
     A review with refs. on the application of the patch clamp method for real
AΒ
     time quant. of polymeric substances such as .alpha.-
     hemolysin protein which can not pass through the channel
     pore by measuring the channel current through interaction with the
     polyethylene glycol (PEG) chain in the channel pore. A diagram
     for quant. of .alpha.-hemolysin using interaction
     between biotinylated PEG with streptavidin was given.
ST
     review channel current patch clamp method
TT
     Electric current
        (channel; microfinishing of channel pore and real time
        sensing)
ΙT
     Biosensors
        (microfinishing of channel pore and real time sensing)
ፐጥ
     Biopolymers
     Ion channel
     RL: ANT (Analyte); ANST (Analytical study)
        (microfinishing of channel pore and real time sensing)
TΤ
     Polyoxyalkylenes, uses
     RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
        (microfinishing of channel pore and real time sensing)
TΤ
     Hemolysins
```

RL: ANT (Analyte); ANST (Analytical study)

```
(.alpha.-; microfinishing of channel pore and real
        time sensing)
     25322-68-3, Polyethylene glycol
ΙT
     RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
        (microfinishing of channel pore and real time sensing)
     ANSWER 7 OF 24 HCAPLUS COPYRIGHT 2002 ACS
1.82
     2001:73166 HCAPLUS
ΑN
     134:277064
DN
     Capture of a single molecule in a nanocavity
ΤI
ΑIJ
     Gu, Li-Qun; Cheley, Stephen; Bayley, Hagan
     Department of Medical Biochemistry and Genetics, Texas A&M University
CS
     System Health Science Center, College Station, TX, 77843, USA
     Science (Washington, DC, United States) (2001), 291(5504), 636-640
SO
     CODEN: SCIEAS; ISSN: 0036-8075
     American Association for the Advancement of Science
PB
DT
     Journal
LA
     English
CC
     6-3 (General Biochemistry)
AΒ
     We describe a heptameric protein pore that has been
     engineered to accommodate two different cyclodextrin adapters
     simultaneously within the lumen of a transmembrane .beta. barrel. The
     vol. between the adapters is a cavity of .apprx.4400 cubic angstroms.
     Anal. of single-channel recordings reveals that individual charged org.
     mols. can be pulled into the cavity by an elec. potential. Once trapped,
     an org. mol. shuttles back and forth between the adapters for hundreds of
     milliseconds. Such self-assembling nanostructures are of interest for the
     fabrication of multianalyte sensors and could provide a means to
     control chem. reactions.
ST
     hemolysin pore self assembling nanostructure mol
     capture
ΙT
     Nanostructures
        (capture of a single mol. in a nanocavity)
TT
     Self-assembly
        (capture of a single mol. in self-assembling nanostructure)
TT
     Electric potential
        (elec. potential pulls charged org. mols. into nanocavity in engineered
        protein pore)
IT
     Free energy of activation
        (free energies of activation for interaction of 1,3-adamantane
        dicarboxylic acid with cyclodextrins lodged within engineered
        protein pore)
ΙT
     Dissociation constant
        (kinetics of cyclodextrin adapters assocn. with .alpha.-
        hemolysin)
ΙT
     Hemolysins
     RL: BPR (Biological process); BSU (Biological study, unclassified); PRP
     (Properties); BIOL (Biological study); PROC (Process)
        (.alpha.-; capture of a single mol. in nanocavity formed in
        .alpha.-hemolysin M113N/N139Q)
ΤT
     70-47-3, L-Asparagine, properties
     RL: PRP (Properties)
        (hepta-6-sulfato-.beta.-cyclodextrin assocs. with Asn139 in
         alpha.-hemolysin)
     5511-18-2, 1-Adamantane carboxamide
                                           39269-10-8, 1,3-Adamantane
ΙT
     dicarboxylic acid
     RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL
     (Biological study); PROC (Process)
        (org. mol. shuttles back and forth between cyclodextrin adapters
        trapped in engineered protein pore)
                                     184840-97-9
ΙT
     7585-39-9, .beta.-Cyclodextrin
     RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL
     (Biological study); PROC (Process)
         (protein pore engineered to accommodate two
        different cyclodextrin adapters)
     63-68-3, L-Methionine, properties
TΤ
```

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RL: PRP (Properties)
        (.beta.-cyclodextrin assocs. with Met113 in .alpha.-
        hemolysin)
RE.CNT
       19
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L82 ANSWER 8 OF 24 HCAPLUS COPYRIGHT 2002 ACS
    2000:737319 HCAPLUS
AN
DN
    134:53412
     Detecting protein analytes that modulate transmembrane movement
    of a polymer chain within a single protein pore
ΑU
    Movileanu, Liviu; Howorka, Stefan; Braha, Orit;
    Bayley, Hagan
    Department of Medical Biochemistry and Genetics, The Texas A&M University
CS
    System Health Science Center, College Station, TX, 77843-1114, USA
    Nature Biotechnology (2000), 18(10), 1091-1095
    CODEN: NABIF9; ISSN: 1087-0156
PR
    Nature America Inc.
DT
    Journal
LA
    English
CC
     9-15 (Biochemical Methods)
     Here we describe a new type of biosensor element for detecting
    proteins in soln. at nanomolar concns. We tethered a 3.4 kDa
    polyethylene glycol chain at a defined site within the lumen of the
     transmembrane protein pore formed by
     staphylococcal .alpha.-hemolysin. The free
     end of the polymer was covalently attached to a biotin mol.
     incorporation of the modified pore into a lipid bilayer, the
    biotinyl group moves from one side of the membrane to the other, and is
    detected by reversible capture with a mutant streptavidin. The capture
     events are obsd. as changes in ionic current passing through single
    pores in planar bilayers. Accordingly, the modified pore
     allows detection of a protein analyte at the single-mol. level,
     facilitating both quantification and identification through a distinctive
     current signature. The approach has higher time resoln. compared with
     other kinetic measurements, such as those obtained by surface plasmon
     resonance.
    protein detection hemolysin polymer chain biotin;
    membrane hemolysin polymer chain protein detection
TΤ
    Membrane, biological
        (bilayer; detecting proteins at nanomolar concns. using
        .alpha.-hemolysin with covalently attached
        polyethylene glycol and biotin)
IT
     Proteins, specific or class
     RL: ANT (Analyte); ANST (Analytical study)
        (biotin-binding; detecting proteins at nanomolar concns.
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using .alpha.-hemolysin with covalently attached

```
polyethylene glycol and biotin)
     Polyoxyalkylenes, biological studies
IT
    RL: BUU (Biological use, unclassified); BIOL (Biological study); USES
        (detecting proteins at nanomolar concns. using
        .alpha.-hemolysin with covalently attached
        polyethylene glycol and biotin)
IT
     Electric current
        (ionic, biol.; detecting proteins at nanomolar concns. using
        .alpha.-hemolysin with covalently attached
        polyethylene glycol and biotin)
IT
     Hemolysins
     RL: BUU (Biological use, unclassified); BIOL (Biological study); USES
     (Uses)
        (.alpha.-; detecting proteins at nanomolar concns.
        using .alpha.-hemolysin with covalently attached
        polyethylene glycol and biotin)
     9013-20-1, Streptavidin
     RL: ANT (Analyte); BAC (Biological activity or effector, except adverse);
     BSU (Biological study, unclassified); ANST (Analytical study); BIOL
     (Biological study)
        (detecting proteins at nanomolar concns. using
        .alpha.-hemolysin with covalently attached
        polyethylene glycol and biotin)
     58-85-5, Biotin 25322-68-3, Polyethylene glycol
ΙT
     RL: BUU (Biological use, unclassified); BIOL (Biological study); USES
        (detecting proteins at nanomolar concns. using
        .alpha.-hemolysin with covalently attached
        polyethylene glycol and biotin)
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L82
     2000:729252 HCAPLUS
ΑN
     134:52844
DN
     Interaction of the noncovalent molecular adapter, .beta.-cyclodextrin,
TΙ
     with the staphylococcal .alpha.-hemolysin
     Gu, Li-Qun; Bayley, Hagan
ΑIJ
     Department of Medical Biochemistry and Genetics, The Texas A and M
CS
     University System Health Science Center, College Station, TX, 77843-1114,
     Biophysical Journal (2000), 79(4), 1967-1975
SO
     CODEN: BIOJAU; ISSN: 0006-3495
     Biophysical Society
PB
     Journal
DT
     English
LA
     6-3 (General Biochemistry)
     Cyclodextrins act as noncovalent mol. adapters when lodged in the lumen of
CC
     the .alpha.-hemolysin (.alpha.HL)
     pore. The adapters act as binding sites for channel blockers,
     thereby offering a basis for the detection of a variety of org. mols. with
     .alpha.HL as a biosensor element. To further such
     studies, it is important to find conditions under which the dwell time of
     cyclodextrins in the lumen of the pore is extended. Here, we
     use single-channel recording to explore the pH- and voltage-dependence of
     the interaction of .beta.-cyclodextrin (.beta.CD) with .alpha
     .HL. .beta.CD can access its binding site only from the trans entrance of
     pores inserted from the cis side of a bilayer. Anal. of the
     binding kinetics shows that there is a single binding site for .beta.CD,
     with an apparent equil. dissocn. const. that varies by >100-fold under the
     conditions explored. The dissocn. rate const. for the neutral .beta.CD
     mol. varies with pH and voltage, a result that is incompatible with two
      states of the .alpha.HL pore, one of high and the
     other of low affinity. Rather, the data suggest that the actual equil.
     dissocn. const. for the .alpha.HL .cntdot. .beta.CD complex
      varies continuously with the transmembrane potential.
     hemolysin alpha pore Staphylococcus
 ST
      interaction beta cyclodextrin
      Membrane, biological
         (bilayer; .beta.-cyclodextrin can access its .alpha.-
        hemolysin binding site only from trans entrance of
         pores inserted from cis side of bilayer)
      Membrane potential
         (biol.; equil. dissocn. const. for .alpha.HL.cntdot..beta.CD complex
         varies continuously with transmembrane potential)
 IT
      Pore
        Staphylococcus aureus
         (interaction of .beta.-cyclodextrin with Staphylococcal
         .alpha.-hemolysin pore)
      Hemolysins
 TT
      RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL
      (Biological study); PROC (Process)
         (.alpha.-; interaction of .beta.-cyclodextrin with
         Staphylococcal .alpha.-hemolysin
         pore)
      7585-39-9, .beta.-Cyclodextrin
      RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL
 IT
       (Biological study); PROC (Process)
         (interaction of .beta.-cyclodextrin with Staphylococcal
          .alpha.-hemolysin pore)
               THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD
 RE.CNT 40
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RE

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 - Stochastic sensing is an emerging anal. technique that relies upon single-mol. detection. Transmembrane pores, into which binding sites for analytes have been placed by genetic engineering, have been developed as stochastic sensing elements. Reversible occupation of an engineered binding site modulates the ionic current passing through a pore in a transmembrane potential and thereby provides both the concn. of an analyte and, through a characteristic signature, its identity. Here, we show that the concns. of two or more divalent metal ions in soln. can be detd. simultaneously with a single sensor element. Further, the sensor element can be permanently

```
calibrated without a detailed understanding of the kinetics of interaction
     of the metal ions with the engineered pore.
     stochastic sensing divalent metal ion
ST
ΙT
     Pore
        (Transmembrane; simultaneous stochastic sensing of divalent metal ions)
     Ion channel
TT
     RL: ANT (Analyte); ANST (Analytical study)
        (Transmembrane; simultaneous stochastic sensing of divalent metal ions)
ΙT
        (divalent; simultaneous stochastic sensing of divalent metal ions)
     Hemolysins
IT
     RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
        (.alpha.-; simultaneous stochastic sensing of divalent metal
        ions)
                                                                   23713-49-7,
                             22537-48-0, Cadmium ion, analysis
     15158-11-9, analysis
ΙT
     Zinc ion, analysis
     RL: ANT (Analyte); ANST (Analytical study)
        (simultaneous stochastic sensing of divalent metal ions)
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      2000:410575 HCAPLUS
 ΑN
      133:189996
 DN
      Resistive-Pulse Sensing-From Microbes to Molecules
 ΤI
      Bayley, Hagan; Martin, Charles R.
 ΑU
      Department of Medical Biochemistry and Genetics, Texas A&M University
      System Health Science Center, College Station, TX, 77843-1114, USA Chem. Rev. (Washington, D. C.) (2000), 100(7), 2575-2594
 SO
      CODEN: CHREAY; ISSN: 0009-2665
      American Chemical Society
 PB
      Journal; General Review
 DT
      English
 LA
      9-0 (Biochemical Methods)
      A review with 173 refs. In this review we attempted to unify various
 CC
      apparently disparate sensing strategies. The unifying feature is the
      underlying measurement principle which entails occlusions of an aperture
      through which a current is passing by the analyte species. While we began
      with a classical and a com. available device, the review focused on two
      very recent manifestations of this sensing paradigm-the use of
      protein-based channels and nanotube membranes for small mol. and
       ion sensing.
       review pulse sensing microbe mol
 ST
       Membrane, biological
 ΙT
       Nanotubes
         Sensors
          (resistive-pulse sensing-from microbes to mols.)
```

Ion channel

IT

```
Proteins, general, properties
    RL: PEP (Physical, engineering or chemical process); PRP (Properties);
    PROC (Process)
        (resistive-pulse sensing-from microbes to mols.)
             THERE ARE 173 CITED REFERENCES AVAILABLE FOR THIS RECORD
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      2000:213198 HCAPLUS
 AN
      132:326109
 DN
      Stochastic sensing of organic analytes by a pore-forming
      protein containing a molecular adapter
      Schultzberg, Maria; Boulin, Christian; Dandekar, Thomas
      European Molecular Biology Laboratory (EMBL), Heidelberg, Germany
 CS
      Chemtracts (2000), 13(3), 198-202
 SO
      CODEN: CHEMFW; ISSN: 1431-9268
      Springer-Verlag New York Inc.
       Journal; General Review
 DT
 LA
       English
       64-1 (Pharmaceutical Analysis)
```

commentary; 15 refs. review hemolysin biosensor; hemolysin biosensor review; biosensor hemolysin review

The title research of Li-Qun Gu, et al. (1999) is reviewed with

Section cross-reference(s): 9

```
IT
    Biosensors
        (stochastic sensing of org. analytes by a pore-forming
        protein contg. mol. adapter)
TΤ
     RL: BSU (Biological study, unclassified); BIOL (Biological study)
        (.alpha.-; stochastic sensing of org. analytes by a
        pore-forming protein contg. mol. adapter)
              THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE.CNT 15
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(15) Walker, B; Protein Eng 1994, V7, P655 HCAPLUS
L82 ANSWER 13 OF 24 HCAPLUS COPYRIGHT 2002 ACS
     2000:136032 HCAPLUS
AN
DN
     132:276277
     A Protein Pore with a Single Polymer Chain Tethered
      within the Lumen
     Howorka, Stefan; Movileanu, Liviu; Lu, Xiaofeng;
ΑU
     Magnon, Melissa; Cheley, Stephen; Braha, Orit; Bayley, Hagan
     Department of Medical Biochemistry & Genetics, Texas A&M Health Science
 CS
      Center, College Station, TX, 77843-1114, USA
      J. Am. Chem. Soc. (2000), 122(11), 2411-2416
 SO
      CODEN: JACSAT; ISSN: 0002-7863
      American Chemical Society
 PB
 DT
      Journal
 LA
     English
      9-16 (Biochemical Methods)
 CC
      A transmembrane protein pore with a single 5000 Da
      poly(ethylene glycol) (PEG) mol. attached covalently within the channel
      lumen has been constructed from seven staphylococcal .
      alpha.-hemolysin subunits. The modified heptamer is
      stable and can be purified by electrophoresis in sodium dodecyl sulfate,
      without dissocn. of the subunits. The properties of the modified
      pore were studied by single channel current recording. The PEG
      mol. reduces the mean conductance of the pore by 18%, as would
      be predicted from the effects of PEG on the cond. of bulk electrolytes.
      The recordings also reveal a variety of low amplitude current fluctuations
      on a time scale of seconds, which are tentatively ascribed to the
      reorganization of the PEG mol. within the channel lumen and assocd.
      movements of the polypeptide chain. Another class of events,
      comprising uniform high-amplitude neg. fluctuations in current with
      durations of milliseconds, is ascribed to motions of the PEG mol. into one
      of the channel entrances, thereby producing more extensive channel block.
      When instead a 3000 Da PEG is attached within the channel lumen, the
      single channel properties are changed in keeping with the lower mass of
      the polymer. For example, the high-amplitude fluctuations occur more
      frequently and are of shorter duration suggesting that the 3000 Da PEG is
      more mobile than the 5000 Da chain. With further development, the
      approach taken here should be useful for the indirect monitoring of
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polymer dynamics at the single mol. level. By using polymers that respond

to analytes, it should also be possible to make biosensors from

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glycol protein pore
     Electric conductivity
IT
     Electric current
        (biol.; heptameric transmembrane protein pore
        constructed with hemolysin subunits and contains
        poly(ethylene glycol) chain tethered to pore lumen)
     Electrolytes, biological
ΙT
        (heptameric transmembrane protein pore constructed
        with hemolysin subunits and contains poly(ethylene glycol)
        chain tethered to pore lumen)
     Polyoxyalkylenes, biological studies
ΙT
     RL: BAC (Biological activity or effector, except adverse); BUU (Biological
     use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
        (heptameric transmembrane protein pore constructed
        with hemolysin subunits and contains poly(ethylene glycol)
        chain tethered to pore lumen)
     Proteins, specific or class
ΙT
     RL: BAC (Biological activity or effector, except adverse); BUU (Biological
     use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
         (transmembrane, pore; heptameric transmembrane
        protein pore constructed with hemolysin
        subunits and contains poly(ethylene glycol) chain tethered to
        pore lumen)
     Hemolysins
TΤ
     RL: BAC (Biological activity or effector, except adverse); BUU (Biological
     use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
         (.alpha.-; heptameric transmembrane protein
        pore constructed with hemolysin subunits and contains
         poly(ethylene glycol) chain tethered to pore lumen)
     25322-68-3, Poly(ethylene glycol)
ፐጥ
     RL: BAC (Biological activity or effector, except adverse); BUU (Biological
     use, unclassified); PRP (Properties); BIOL (Biological study); USES (Úses)
         (heptameric transmembrane protein pore constructed
         with hemolysin subunits and contains poly(ethylene glycol)
         chain tethered to pore lumen)
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L82 ANSWER 14 OF 24 HCAPLUS COPYRIGHT 2002 ACS
     2000:62780 HCAPLUS
AN
DN
     132:104791
ΤI
     Stochastic sensing with protein pores
     Bayley, Hagan; Braha, Orit; Gu, Li-Qun
ΑU
     Dep. Medical Biochem. Genetics, Texas A & M Health Science Center, College
CS
     Station, TX, 77843, USA
     Adv. Mater. (Weinheim, Ger.) (2000), 12(2), 139-142
SO
     CODEN: ADVMEW; ISSN: 0935-9648
PB
     Wiley-VCH Verlag GmbH
DT
     Journal; General Review
LA
     English
CC
     9-0 (Biochemical Methods)
     A review with 28 refs. is given on the use of engineered transmembrane
AB
     protein pores as stochastic biosensor elements
     including natural ion channels as sensors, and the genetically
     engineered staphylococcal .alpha.-hemolysin
     for the detection of metals and with a cyclodextrin-modified
     protein pore for the detection of org. mols.
     review biosensor protein pore metal detn;
ST
     org substance biosensor protein pore review;
     ion channel biosensor review
     Proteins, general, analysis
     RL: ARU (Analytical role, unclassified); DEV (Device component use); ANST
     (Analytical study); USES (Uses)
         (cyclodextrin-modified; stochastic sensing with protein
        pores)
ΙT
     Biosensors
         (stochastic sensing with protein pores)
IT
     Metals, analysis
     Organic compounds, analysis
     RL: ANT (Analyte); ANST (Analytical study)
         (stochastic sensing with protein pores)
ΙT
     Ion channel
     RL: ARU (Analytical role, unclassified); DEV (Device component use); ANST
     (Analytical study); USES (Uses)
         (stochastic sensing with protein pores)
ΙT
     Hemolysins
     RL: ARU (Analytical role, unclassified); DEV (Device component use); ANST
      (Analytical study); USES (Uses)
         (.alpha.-, bacterial; stochastic sensing with protein
        pores)
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RE.CNT
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- L82 ANSWER 15 OF 24 HCAPLUS COPYRIGHT 2002 ACS
- AN 1999:283318 HCAPLUS
- DN 131:92613
- TI Stochastic sensing of organic analytes by a pore-forming protein containing a molecular adapter
- AU Gu, Li-Qun; Braha, Orit; Conlan, Sean; Cheley, Stephen; Bayley,
- CS Department of Medical Biochemistry & Genetics, Texas A&M University Health Science Center, College Station, TX, 77843-1114, USA
- SO Nature (London) (1999), 398(6729), 686-690 CODEN: NATUAS; ISSN: 0028-0836
- PB Macmillan Magazines
- DT Journal
- LA English
- CC 64-3 (Pharmaceutical Analysis)
- AB The detection of org. mols. is important in many areas, including medicine, environmental monitoring and defense. Stochastic sensing is an approach that relies on the observation of individual binding events between analyte mols. and a single receptor. Engineered transmembrane protein pores are promising sensor elements

for stochastic detection, and in their simplest manifestation they produce a fluctuating binary ('on/off') response in the transmembrane elec. current. The frequency of occurrence of the fluctuations reveals the concn. of the analyte, and its identity can be deduced from the characteristic magnitude and/or duration of the fluctuations. Genetically engineered versions of the bacterial pore-forming

protein .alpha.-hemolysin have been used to

identify the quantify divalent metal ions in soln. But it is not immediately obvious how versatile binding sites for org. ligands might be obtained by engineering of the **pore** structure. Here we show that stochastic sensing of org. mols. can be procured from .alpha

.-hemolysin by equipping the channel with an internal,

non-covalently bound mol. 'adapter' which mediates channel blocking by the analyte. We use cyclodextrins as the adapters because these fit comfortably inside the **pore** and present a hydrophobic cavity suitable for binding a variety of org. analytes. Moreover, a single sensing element of this sort can be used to analyze a mixt. of org. mols.

sensing element of this sort can be used to analyze a mixt. Of org. Mo. with different binding characteristics. We envisage the use of other adapters, so that the **pore** could be 'programmed' for a range of

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sensing functions.
ST
     hemolysin cyclodextrin adapter biosensor org compd;
     drug analysis biosensor hemolysin cyclodextrin
IT
     Biosensors
     Pharmaceutical analysis
        (stochastic sensing of org. analytes by pore-forming
        .alpha.-hemolysin contg. cyclodextrin as mol.
        adapter)
IT
     Hemolysins
     RL: ARU (Analytical role, unclassified); ANST (Analytical study)
        (.alpha.-; stochastic sensing of org. analytes by
        pore-forming .alpha.-hemolysin contg.
        cyclodextrin as mol. adapter)
     50-49-7, Imipramine 60-87-7, Promethazine
IΤ
                                                    828-51-3,
     1-Adamantanecarboxylic acid
                                  13074-39-0, 2-Adamantanamine
     RL: ANT (Analyte); ANST (Analytical study)
        (stochastic sensing of org. analytes by pore-forming
        .alpha.-hemolysin contq. cyclodextrin as mol.
        adapter)
     7585-39-9, .beta.-Cyclodextrin 12619-70-4, Cyclodextrin
ΙT
     RL: ARU (Analytical role, unclassified); MOA (Modifier or additive use);
     ANST (Analytical study); USES (Uses)
        (stochastic sensing of org. analytes by pore-forming
        .alpha.-hemolysin contg. cyclodextrin as mol.
        adapter)
RE.CNT
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L82
AN
     1999:124048 HCAPLUS
DN
     130:293399
TΤ
     Designed membrane channels and pores
AII
     Bayley, Hagan
     Department of Medical Biochemistry and Genetics, Texas AandM Health
     Science Center, College Station, TX, 77843-1114, USA
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Curr. Opin. Biotechnol. (1999), 10(1), 94-103

SO

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CODEN: CUOBE3; ISSN: 0958-1669
PB
     Current Biology Publications
DT
     Journal; General Review
LA
     English
CC
     9-0 (Biochemical Methods)
     A review with 72 refs. Advances in the synthesis and assembly of designed
AB
     membrane channels and pores include addressable
     template-assisted synthetic protein (TASP) syntheses of helix
     bundles, the prodn. of a new class of nanotubes and the ability to purify
     hetero-oligomeric pores. Channels and pores
     with altered functional properties and with built-in triggers and switches
     have been prepd. Progress in applications has been greatest in
     sensor technol., where sensor elements based on ligand
     activation, channel selectivity and channel block have been made.
     Structural information about natural membrane proteins is
     emerging to inspire new designs.
ST
     review designed membrane channel pore
TΤ
     Membranes (biological)
         (designed membrane channels and pores)
TT
     Ion channel
     RL: ANT (Analyte); ANST (Analytical study)
         (designed membrane channels and pores)
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L82
    ANSWER 17 OF 24 HCAPLUS COPYRIGHT 2002 ACS
ΑN
     1999:96264
                 HCAPLUS
DN
     130:165159
     Designed staphylococcal hemolysin protein
ΤI
     pores as components for metal biosensors
     Bayley, Hagan; Braha, Orit; Kasianowicz, John; Gouaux, Eric
IN
     University of Massachusetts, USA
PA
SO
     PCT Int. Appl., 51 pp.
     CODEN: PIXXD2
DT
     Patent
LA
     English
IC
     ICM C07K014-195
     ICS C07K014-305; C07K014-31; G01N033-20; G01N033-48
     9-7 (Biochemical Methods)
     Section cross-reference(s): 6, 50, 72, 79
FAN.CNT 1
                                             APPLICATION NO.
                                                              DATE
     PATENT NO.
                      KIND DATE
                             19990204
                                             WO 1998-US15354
                                                              19980724
PΙ
     WO 9905167
                       A1
         W: AU, CA, JP, KR
         RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL,
             PT, SE
                                             AU 1998-85862
                                                               19980724
                             19990216
     AU 9885862
                        Α1
PRAI US 1997-53737P
                             19970725
                        Р
     WO 1998-US15354
                        W
                            19980724
     This invention features a mutant staphylococcal alpha
     hemolysin (.alpha.HL) polypeptide contg. a
     heterologous metal-binding amino acid. The polypeptide
     assembles into a heteroheptameric pore assembly in the presence
     of a wild type .alpha.HL polypeptide. Preferably, the
     metal-binding amino acid occupies a position in a transmembrane channel of
     the heteroheptameric pore assembly, e.g., an amino acid in the
     stem domain of WT .alpha.HL is substituted with a heterologous
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metal-binding amino acid. More preferably, the metal-binding amino acid

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projects into the lumen of the transmembrane channel.
     hemolysin staphylococcal peptide mutant
     channel pore metal biosensor
IT
    Biosensors
     Electrodes
     Explosives
     Mutation
       Pore
       Pore structure
       Protein sequences
     Quaternary structure (protein)
     Self-association
       Staphylococcus
        (designed staphylococcal hemolysin protein
        pores as components for metal biosensors)
ፐጥ
     Metals, analysis
     Organic compounds, analysis
     RL: ANT (Analyte); BPR (Biological process); ANST (Analytical study); BIOL
     (Biological study); PROC (Process)
        (designed staphylococcal hemolysin protein
        pores as components for metal biosensors)
ΙT
     Amino acids, analysis
     RL: ARU (Analytical role, unclassified); BPR (Biological process); BSU
     (Biological study, unclassified); BUU (Biological use, unclassified); DEV
     (Device component use); ANST (Analytical study); BIOL (Biological study);
     PROC (Process); USES (Uses)
        (designed staphylococcal hemolysin protein
        pores as components for metal biosensors)
     RL: ARU (Analytical role, unclassified); BPR (Biological process); BSU
     (Biological study, unclassified); BUU (Biological use, unclassified); DEV
     (Device component use); PRP (Properties); ANST (Analytical study); BIOL
     (Biological study); PROC (Process); USES (Uses)
        (designed staphylococcal hemolysin protein
        pores as components for metal biosensors)
     .alpha.-Hemolysins
     RL: ARU (Analytical role, unclassified); BUU (Biological use,
     unclassified); DEV (Device component use); PRP (Properties); ANST
     (Analytical study); BIOL (Biological study); USES (Uses)
        (designed staphylococcal hemolysin protein
        pores as components for metal biosensors)
     Diffusion
TT
        (pore; designed staphylococcal hemolysin
        protein pores as components for metal
        biosensors)
                                220376-65-8
                  220376-64-7
TΤ
     220376-63-6
     RL: ARU (Analytical role, unclassified); BUU (Biological use,
     unclassified); DEV (Device component use); PRP (Properties); ANST
     (Analytical study); BIOL (Biological study); USES (Uses)
        (amino acid sequence; designed staphylococcal
        hemolysin protein pores as components for
        metal biosensors)
                                   7440-43-9, Cadmium, analysis 7440-48-4, Copper, analysis 7440-66-6, Zinc, analysis
     7440-02-0, Nickel, analysis
                        7440-50-8, Copper, analysis
     Cobalt, analysis
     14701-22-5, Nickel(2+), analysis 15158-11-9, Copper(2+), analysis
                                        22541-53-3, Cobalt(2+), analysis
     22537-48-0, Cadmium(2+), analysis
     23713-49-7, Zinc(2+), analysis
     RL: ANT (Analyte); BPR (Biological process); ANST (Analytical study); BIOL
     (Biological study); PROC (Process)
        (designed staphylococcal hemolysin protein
        pores as components for metal biosensors)
                                     56-45-1, L-Serine, analysis
                                                                    56-84-8,
     52-90-4, L-Cysteine, analysis
     L-Aspartic acid, analysis 56-86-0, L-Glutamic acid, analysis 60-18-4,
                            63-68-3, L-Methionine, analysis 71-00-1,
     L-Tyrosine, analysis
     L-Histidine, analysis
                             72-19-5, L-Threonine, analysis
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L-Tryptophan, analysis

RL: ARU (Analytical role, unclassified); BUU (Biological use,

unclassified); DEV (Device component use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses) (designed staphylococcal hemolysin protein pores as components for metal biosensors) THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD RE.CNT RE (1) Bayley; US 5777078 A 1998 HCAPLUS L82 ANSWER 18 OF 24 HCAPLUS COPYRIGHT 2002 ACS AN 1999:74251 HCAPLUS 130:248484 DN Genetically engineered metal ion binding sites on the outside of a ΤI channel's transmembrane .beta.-barrel Kasianowicz, John J.; Burden, Daniel L.; Han, Linda C.; Cheley, Stephen; Bayley, Hagan Biotechnology Division, National Institute of Standards and Technology, CS Gaithersburg, MD, 20899, USA Biophys. J. (1999), 76(2), 837-845 SO CODEN: BIOJAU; ISSN: 0006-3495 PB Biophysical Society DT Journal LA English CC 6-3 (General Biochemistry) We are exploring the ability of genetically engineered versions of the Staphylococcus aureus .alpha.hemolysin (.alpha.HL) ion channel to serve as rationally designed sensor components for analytes including divalent cations. We show here that neither the hemolytic activity nor the single channel current of wild-type .alpha.HL was affected by [Zn(II)] .ltoreq.1 mM. Binding sites for the divalent cations were formed by altering the no. and location of coordinating side chains, e.g., histidines and aspartic acids, between positions 126 and 134, inclusive. Several mutant .alpha.HLs exhibited Zn(II)-induced current noise that varied with Zn(II) concn. At a fixed divalent cation concn., the current fluctuation kinetics depended on the analyte type, e.g., Zn(II), Cu(II), Ni(II), and Co(II). We also show that the ability of Zn(II) to change the mutant channel current suggests that the pore's topol. is .beta.-sheet and that position 130 is near the turn at the trans mouth. Both conclusions are consistent with the crystal structure of WT-. alpha. HL oligomerized in detergent. Our results, in the context of the channel's crystal structure, suggest that conductance blockades were caused by Zn(II) binding to the outside surface of the pore. Thus, analyte-induced current blockades alone might not establish whether an analyte binding site is inside a pore. hemolysin ion channel engineered divalent cation sensor ΙT Electric conductivity (biological) Protein engineering .beta.-Barrel (genetically engineered metal ion binding sites on outside of a channel's transmembrane .beta.-barrel) .alpha.-Hemolysins RL: BPR (Biological process); BIOL (Biological study); PROC (Process) (genetically engineered metal ion binding sites on outside of a channel's transmembrane .beta.-barrel) 7440-48-4, Cobalt, biological ΙT 7440-02-0, Nickel, biological studies 7440-50-8, Copper, biological studies 7440-66-6, Zinc, studies biological studies RL: BPR (Biological process); BIOL (Biological study); PROC (Process) (genetically engineered metal ion binding sites on outside of a channel's transmembrane .beta.-barrel) THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD RE.CNT (1) Akabas, M; Biochemistry 1992, V34, P12496 (2) Akabas, M; Science 1992, V258, P307 HCAPLUS

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1.82
     1997:545947 HCAPLUS
AN
DN
     127:217192
     Designed protein pores as components for
     biosensors
     Braha, Orit; Walker, Barbara; Cheley, Stephen; Kasianowicz, John J.; Song,
ΑIJ
     Langzhou; Gouaux, J. Eric; Bayley, Hagan
     Department of Medical Biochemistry and Genetics, Texas AandM Health
CS
     Science Center, College Station, TX, 77843-1114, USA
     Chem. Biol. (1997), 4(7), 497-505
     CODEN: CBOLE2; ISSN: 1074-5521
PB
     Current Biology
DT
     Journal
LA
     English
CC
     9-1 (Biochemical Methods)
     There is a pressing need for new sensors that can detect a
     variety of analytes, ranging from simple ions to complex compds. and even
     microorganisms. The devices should offer sensitivity, speed,
     reversibility and selectivity. Given these criteria, protein
     pores, remodeled so that their transmembrane conductances are
     modulated by the assocn. of specific analytes, are excellent prospects as
     components of biosensors. Structure-based design and a sepn.
     method that employs targeted chem. modification have been used to obtain a
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heteromeric form of the bacterial pore-forming protein

of the seven subunits contains a binding site for a divalent metal ion, M(II), which serves as a prototypic analyte. The single-channel current

staphylococcal .alpha.-hemolysin, in which one

of the heteromer in planar bilayers is modulated by nanomolar Zn(II). Other M(II)s modulate the current and produce characteristic signatures. In addn., heteromers contg. more than one mutant subunit exhibit distinct responses to M(II)s. Hence, a large collection of responsive pores can be generated through subunit diversity and combinatorial assembly. Engineered pores have several advantages as potential sensor elements: sensitivity is in the nanomolar range; analyte binding is rapid (diffusion limited in some cases) and reversible; strictly selective binding is not required because single-channel recordings are rich in information; and for a particular analyte, the dissocn. rate const., the extent of channel block and the voltage-dependence of these parameters are distinguishing, while the frequency of partial channel block reflects the analyte concn. A single sensor element might, therefore, be used to quantitate more than one analyte at once. The approach described here can be generalized for addnl. analytes. protein pore biosensor Biosensors (designed protein pores as components for biosensors) Proteins (general), uses .alpha.-Hemolysins RL: DEV (Device component use); USES (Uses) (designed protein pores as components for biosensors) L82 ANSWER 20 OF 24 HCAPLUS COPYRIGHT 2002 ACS 1996:304450 HCAPLUS 124:335771 Pore-forming proteins with built-in triggers and switches Bayley, Hagan Worcester Foundation for Biomedical Research, Shrewsbury, MA, 01545, USA Proc. SPIE-Int. Soc. Opt. Eng. (1996), 2716(Smart Materials Technologies and Biomimetics), 313-316 CODEN: PSISDG; ISSN: 0277-786X Journal; General Review English 6-0 (General Biochemistry) Section cross-reference(s): 3 A review, with 9 refs. Genetic engineering and targeted chem. modification are being used to produce polypeptides with pore-forming activity that can be triggered or switched on-and-off by biochem., chem. or phys. stimuli. The principal target of our studies has been the .alpha.-hemolysin (.alpha.HL) from the bacterium Staphylococcus aureus. remodeled hemolysins include protease-activated pores, metal-regulated pores, pores that are activated by chem. alkylation and pores that are turned on with light. These polypeptides have several potential applications. For example, they might serve as components of sensors or they might be useful for mediating the controlled release of encapsulated drugs. protein pore forming hemolysin alpha review Proteins, specific or class RL: PNU (Preparation, unclassified); PRP (Properties); PREP (Preparation) (pore-forming, pore-forming proteins with built-in triggers and switches) Hemolysins RL: PNU (Preparation, unclassified); PRP (Properties); PREP (Preparation) (.alpha.-, pore-forming proteins with built-in triggers and switches)

ANSWER 21 OF 24 HCAPLUS COPYRIGHT 2002 ACS

1996:48968 HCAPLUS

124:109804

ST

TΤ

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DT

LA

CC

ST

ΙT

ΙT

L82

DN

```
Pore-forming proteins with built-in triggers and
ΤI
    switches
ΑU
    Bayley, Hagan
    Worcester Foundation Biomedical Research, Shrewsbury, MA, 01545, USA
CS
    Bioorg. Chem. (1995), 23(4), 340-54
SO
    CODEN: BOCMBM; ISSN: 0045-2068
DT
    Journal; General Review
    English
LA
     6-0 (General Biochemistry)
CC
    A review, with 72 refs. The self-assembling, pore-forming
AB.
    protein .alpha.-hemolysin is a monomeric,
     293-amino-acid, water-sol. polypeptide that forms heptameric
    pores of 1- to 2-nm internal diam. in lipid bilayers. By genetic
     engineering and targeted chem. modification, the authors have produced .
     alpha.-hemolysin in which pore-forming
     activity can be triggered or switched on and off by biochem., chem., or
     phys. stimuli. These remodeled mols. include protease-activated
     pores, metal-regulated pores, pores that are
     activated by chem. alkylation, and pores that are turned on with
     light. Engineered .alpha.-hemolysins have potential
     applications that include acting as components of sensors for
     various analytes, mediating the controlled release of drugs and forming
     building blocks for agents that selectivity damage malignant cells.
     hemolysin alpha pore review
ΤT
     Hemolysins
     RL: BPR (Biological process); PRP (Properties); BIOL (Biological study);
     PROC (Process)
        (.alpha.-, pore-forming proteins with
        built-in triggers and switches)
L82 ANSWER 22 OF 24 HCAPLUS COPYRIGHT 2002 ACS
     1995:77803 HCAPLUS
ΑN
     122:182287
DN
     Genetically engineered pores as metal biosensors
TΙ
     Kasianowicz, John; Walker, Barbara; Krishnasastry, Musti; Bayley,
AU
     Biotechnology Division, NIST, Gaithersburg, MD, 20899, USA
CS
     Mater. Res. Soc. Symp. Proc. (1994), 330 (Biomolecular Materials by
SO
     Design), 217-23
     CODEN: MRSPDH; ISSN: 0272-9172
DT
     Journal
LA
     English
     9-2 (Biochemical Methods)
CC
     Section cross-reference(s): 3
     The authors are adapting proteins that form pores in
AB
     lipid bilayers for use as components of biosensors.
     Specifically, the authors have produced genetically engineered variants of
     the .alpha.-hemolysin (.alpha.{\tt HL}) from
     Staphylococcus aureus with properties that are sensitive
      to low concns. of divalent cations. For example, the pore
      -forming activity of one mutant (.alpha.HL-H5: residues 130-134
      inclusive replaced with histidine) is inhibited by Zn2+ at concns. as low
      as 1 .mu.M, as judged by the redn. in its ability to lyse rabbit red blood
      cells and to increase the conductance of planar lipid bilayer membranes.
      When .alpha.HL-H5 is added to the aq. phase bathing one side of
      a planar membrane, the subsequent addn. of 100 .mu.M Zn2+ to either side
      blocks the pores that form. This result suggests that at least
      part of the mutated region lines the channel lumen. Ca2+ and Mg2+ do not
      block the channel and therefore the H5 mutation confers a degree of
      analyte specificity to the .alpha.HL pore. The
      results suggest that genetically engineered pores have great
      promise for the rapid and sensitive detection of metal cations and the
      authors discuss the merits and potential limitations for their use in this
      application. Specifically, the authors examine the issues of selectivity,
      sensitivity, response time, dynamic range and longevity. Some of these
      properties are interdependent. For example, the goals of high sensitivity
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and rapid response time can be in conflict.
    genetically engineered pore metal cation biosensor;
ST
    hemolysin pore forming metal cation biosensor
    Biosensors
ፐጥ
        (cation sensitive; genetically engineered pores as metal
       biosensors)
     Genetic engineering
IT
        (genetically engineered pores as metal biosensors)
     Staphylococcus aureus
TΤ
        (hemolysin from; genetically engineered pores as
        metal biosensors)
     Membrane, biological
ΙT
        (bilayer, lipid, pores formed in; genetically engineered
        pores as metal biosensors)
IT
     Cations
        (divalent, genetically engineered pores as metal
        biosensors)
     Proteins, specific or class
IT
     RL: BAC (Biological activity or effector, except adverse); BIOL
     (Biological study)
        (pore-forming, genetically engineered pores as
        metal biosensors)
     Hemolysins
TΤ
     RL: BAC (Biological activity or effector, except adverse); BIOL
     (Biological study)
        (.alpha.-, genetically engineered, pore-forming;
        genetically engineered pores as metal biosensors)
                                                                23713-49-7,
                                 22537-22-0, Mg2+, analysis
     14127-61-8, Ca2+, analysis
IT
     Zn2+, analysis
     RL: ANT (Analyte); ANST (Analytical study)
        (genetically engineered pores as metal biosensors)
L82 ANSWER 23 OF 24 HCAPLUS COPYRIGHT 2002 ACS
     1994:529301 HCAPLUS
ΑN
     121:129301
DN
     A pore-forming protein with a metal-actuated switch
ΤI
     Walker, Barbara; Kasianowicz, John; Krishnasastry, Musti; Bayley,
ΑU
     Worcester Found. Exp. Biol., Shrewsbury, MA, 01545, USA
CS
     Protein Eng. (1994), 7(5), 655-62
 SO
     CODEN: PRENE9; ISSN: 0269-2139
 \mathsf{DT}
     Journal
     English
 LA
     9-16 (Biochemical Methods)
 CC
     Staphylococcal .alpha.-hemolysin, a
     pore-forming exotoxin, is a polypeptide of 293 amino
     acids that is secreted by Staphylococcus aureus as a
      water-sol. monomer. It assembles to form hexameric pores in
     lipid bilayers. Previous studies of pore formation have
     established the involvement of a central glycine-rich loop. Here, the
     authors show that when five consecutive histidine residues replace amino
      acids 130-134 at the midpoint of the loop, they provide a switch with
      which pore activity can be (i) turned off by micromolar concns.
      of divalent zinc ions and (ii) turned back on with the chelating agent
      EDTA. Planar bilayer recordings show that Zn2+ and EDTA can act on open
      channels from either side of the bilayer and thus demonstrate that the
      central loop lines part of the conductive pathway. The authors' results
      suggest that genetically-engineered pore-forming
      proteins might make useful components of metal ion sensors
      staphylococcal hemolysin metal actuated switch; zinc
      protein histidine metal switch; pore forming
      protein metal switch
      Proteins, specific or class
      RL: ANST (Analytical study)
         (pore-forming, metal-actuated switch in)
```

```
IT
     Staphylococcus aureus
        (.alpha.-hemolysin from, pore
        activity-controlling metal-actuated switch for)
IT
    Hemolysins
     RL: ANST (Analytical study)
        (.alpha.-, staphylococcal, pore
        activity-controlling metal-actuated switch in)
IT
     71-00-1, Histidine, biological studies
     RL: BIOL (Biological study)
        (amino acids in staphylococcal .alpha.-
        hemolysin replaced by, metal-actuated switch in relation to)
IT
    7440-66-6, Zinc, biological studies
     RL: BIOL (Biological study)
        (pore activity-controlling switch response to, in
        staphylococcal .alpha.-hemolysin)
L82 ANSWER 24 OF 24 HCAPLUS COPYRIGHT 2002 ACS
    1993:426821 HCAPLUS
AN
DN
    119:26821
ΤI
    Monolayers from genetically engineered protein pores
ΑU
    Bayley, Hagan
CS
    Worcester Found. Exp. Biol., Shrewsbury, MA, 01545, USA
SO
    Mater. Res. Soc. Symp. Proc. (1991), 218 (Materials Synthesis Based on
    Biological Processes), 69-74
    CODEN: MRSPDH; ISSN: 0272-9172
DT
    Journal
LA
    English
CC
    16-9 (Fermentation and Bioindustrial Chemistry)
    Section cross-reference(s): 3, 6
AB
    A selection of microscopic pores is being made by genetic
    manipulation of a bacterial channel protein, .alpha.-
    hemolysin (.alpha.-HL). It will include: pores
    with different internal diams., with differential selectivity for the
    passage of classes of mols., and with different gating properties.
    pores will be made into monolayers and incorporated into materials
    such as thin films to confer novel permeability properties upon them.
    Such products will have several technol. applications, for example as mol.
     filters in sensors or as components of optically gated devices
    in electronics.
    genetic engineering alpha hemolysin monolayer
    pore
TΤ
    Gene, microbial
    RL: PROC (Process)
        (for .alpha.-hemolysin of Staphylococcus
        aureus, genetic engineering of, for formation of pore
        -contq. monolayers)
TT
    Mutation
        (of .alpha.-hemolysin gene of
        Staphylococcus aureus, for formation of pore
        -contg. monolayers)
IT
    Genetic engineering
       (of .alpha.-hemolysin of Staphylococcus
        aureus, for formation of pore-contg. monolayers)
IT
    Staphylococcus aureus
        (.alpha.-hemolysin of, genetic engineering of, for
        formation of pore-contg. monolayers)
TΤ
    Hemolysins
     RL: PROC (Process)
        (.alpha.-, genetic engineering of, for formation of
        pore-contg. monolayers)
TΤ
    Conformation and Conformers
        (.alpha.-helical, of .alpha.-hemolysin of
        Staphylococcus aureus, pore formation in
        relation to)
ΙT
     Conformation and Conformers
```

(.beta.-bend, of .alpha.-hemolysin of

```
Staphylococcus aureus, pore formation in
         relation to)
 IT
      Conformation and Conformers
         (.beta.-sheet, of .alpha.-hemolysin of
         Staphylococcus aureus, pore formation in
         relation to)
 => d his
      (FILE 'HOME' ENTERED AT 14:25:36 ON 19 MAR 2002)
                 SET COST OFF
      FILE 'BIOSIS' ENTERED AT 14:25:46 ON 19 MAR 2002
                 E BAYLEY H/AU
 L1
             139 S E3, E4, E6
                 E HOWORKA S/AU
 L2
              12 S E3-E5
                 E MOVILEANU L/AU
              25 S E3, E4
L3
             160 S L1-L3
 L4
              15 S L4 AND ?SENSOR?
 L5
L6
              13 S L5 AND ?PORE?
               9 S L5 AND (ALPHA OR ALFA) (L) (HEMOLYSIN? OR HAEMOLYSIN? OR HEAMOL
L7
               9 S L5 AND (HEMOLYSIN? OR HAEMOLYSIN? OR HEAMOLYSIN?)
^{L8}
 L9
               9 S L7, L8 AND L6
 L10
               6 S L5, L6 NOT L9
                 SEL DN AN 5 6
L11
               4 S L10 NOT E1-E4
              13 S L7, L8, L11 AND L1-L11
L12
               8 S L12 AND (?PEPTIDE? OR PROTEIN OR SEQUENC? OR (10054 OR 10064)
L13
               8 S L12 AND STAPHYLOC?
 L14
 L15
              10 S L13, L14
L16
               3 S L12 NOT L15
              13 S L15,L16 AND (?SENSOR? OR ?SENSING OR ?OLIGO?)
L17
L18
               9 S L15, L16 AND ALPHA?
 L19
              13 S L12-L18
      FILE 'HCAPLUS' ENTERED AT 14:35:09 ON 19 MAR 2002
                 E BAYLEY H/AU
L20
             132 S E3, E6-E10
                 E HOWORKA S/AU
              13 S E3, E5-E7
L21
                 E MOVILEANU L/AU
L22
              29 S E3, E4
L23
           14253 S BIOSENS?
L24
          103970 S SENSOR
                 E BIOSENSOR/CT
                 E E4+ALL
L25
           52868 S E6+NT
L26
             329 S E12+NT
L27
          206371 S E5+NT
 L28
              22 S L20-L22 AND L23-L27
 L29
            7543 S PROTEIN(L) PORE
 L30
            1855 S (PEPTIDE OR POLYPEPTIDE) (L) PORE
 L31
            8402 S L29, L30
             932 S (ALPHA OR ALFA) (L) (HEMOLYSIN? OR HAEMOLYSIN? OR HEAMOLYSIN?)
 L32
                 E ALPHA-HEMOLYSIN/CT
                 E E4+ALL
 L33
             355 S E2
                 E E2+ALL
 L34
            3391 S E3
                 E E2+ALL
 L35
            4528 S E2+NT
```

L36

L37

199 S L31 AND L32-L35

52 S L36 AND STAPHYLOC?

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L38
             26 S L37 AND (PROTEIN OR ?PEPTIDE) (5A) PORE
                E STAPHYLOCOCCUS/CT
                E E3+ALL
          24392 S E5+NT
L39
L40
          52623 S E5, E7/BI
          41648 S E8-E85/BI
L41
             39 S L36 AND L39-L41
             18 S L42 AND (PROTEIN OR ?PEPTIDE?) (5A) PORE
L43
             27 S L38, L43
L44
             25 S L37, L42 NOT L44
L45
             20 S L28 AND L29-L45
L46
L47
             19 S L28 AND (HEMOLYSIN? OR HAEMOLYSIN? OR HEAMOLYSIN?)
             12 S L28 AND (STAPHYLOC? OR L39-L41)
L48
L49
             17 S L28 AND (PROTEIN? OR ?PEPTIDE?)
             5 S L28 AND ?OLIGO?
L50
L51
             22 S L28, L46-L50
     FILE 'HCAPLUS, BIOSIS' ENTERED AT 14:54:38 ON 19 MAR 2002
L52
             22 DUP REM L51 L19 (13 DUPLICATES REMOVED)
     FILE 'WPIX' ENTERED AT 14:54:49 ON 19 MAR 2002
L53
         383390 S SENSOR OR BIOSENSOR OR BIO SENSOR
             37 S L53 AND (PROTEIN? OR ?PEPTIDE?) (L) PORE
L54
            217 S L53 AND (B04-C01? OR C04-C01?)/MC
L55
             12 S L55 AND PORE
L56
L57
             40 S L54, L56
                E BAYLEY H/AU
L58
              5 S E3, E6
                E HOWORKA S/AU
L59
              2 S E3, E4
                E MOVILEANU L/AU
L60
              1 S E3
L61
              2 S L53 AND L58-L60
L62
              4 S L57 AND STAPHYLOC?
L63
           1888 S L53 AND ?LYSIN?
L64
              5 S L63 AND L57
              2 S L64 AND (HEMOLYSIN? OR HEAMOLYSIN?) OR HAEMOLYSIN?)
L65
              4 S L61, L62, L65
L66
              2 S L53 AND (HEMOLYSIN? OR HEAMOLYSIN? OR HAEMOLYSIN?)
L67
1.68
              4 S L66, L67
             36 S L57 NOT L68
1.69
                SEL DN AN 24 25 L69
              2 S L69 AND E1-E5
L70
L71
              6 S L68, L70
     FILE 'WPIX' ENTERED AT 15:12:17 ON 19 MAR 2002
     FILE 'HCAPLUS' ENTERED AT 15:12:33 ON 19 MAR 2002
L72
         267465 S L53 OR L23-L27
            154 S L72 AND (?PEPTIDE? OR PROTEIN?) (L) PORE
L73
L74
            151 S L72 AND L31
            154 S L73, L74
1.75
L76
             16 S L75 AND L32-L35
L77
             24 S L51, L76
            201 S L72 AND (?PEPTIDE? OR PROTEIN?) AND PORE
L78
L79
             17 S L32-L35 AND L78
L80
             24 S L77, L79
L81
             23 S L80 AND PORE
L82
             24 S L80-L81
```

FILE 'HCAPLUS' ENTERED AT 15:16:28 ON 19 MAR 2002